

## **RAW SEQUENCE LISTING ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technological Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/530,209

Source: 1638

Date Processed by STIC: 2/27/2001

### **THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

### **PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

# RAW SEQUENCE LISTING

## PATENT APPLICATION US/09/530,209

1638

 #10  
 3/2/01  
 DATE: 02/27/2001  
 TIME: 20:20:22

INPUT SET: S36432.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

 see pp. 6-7

## SEQUENCE LISTING

 Does Not Comply  
 Corrected Diskette Needed

## (1) General Information:

## (i) APPLICANT:

~~(A) NAME: CropDesign NV~~~~(B) STREET: TechnologiePark Zwijnaarde 3~~~~(C) CITY: Gent~~~~(D) STATE: none~~~~(E) COUNTRY: Belgium~~~~(F) POSTAL CODE (ZIP): 9052~~

(ii) TITLE OF INVENTION: A novel mitogenic cyclin and uses thereof

(iii) NUMBER OF SEQUENCES: 4

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

## (vi) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE:

(B) STREET:

(C) CITY:

(D) STATE:

(E) COUNTRY:

(F) ZIP:

## (vii) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 927 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..927

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATG GCA GAG GAA AAT CTA GAA CTG AGT CTT TTA TGT ACA GAG AGC AAC

Met Ala Glu Glu Asn Leu Leu Ser Leu Leu Cys Thr Glu Ser Asn

1

5

10

15

48

46

 add these  
 mandatory  
 headings and  
 responses for  
 a U.S. case

 FYI: EPO format  
 is invalid for a  
U.S. case

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/530,209

DATE: 02/27/2001  
TIME: 20:20:22

INPUT SET: S36432.raw

47	GTT GAT GAT GAG GGC ATG ATT GTT GAC GAA ACT CCG ATT GAA ATT TCG	96
48	Val Asp Asp Glu Gly Met Ile Val Asp Glu Thr Pro Ile Glu Ile Ser	
49	20 25 30	
50		
51	ATT CCT CAG ATG GGT TTT TCT CAA TCG GAG AGT GAG GAG ATT ATC ATG	144
52	Ile Pro Gln Met Gly Phe Ser Gln Ser Glu Ser Glu Glu Ile Ile Met	
53	35 40 45	
54		
55	GAG ATG GTG GAG AAG GAG AAG CAG CAT TTG CCA AGT GAT GAT TAC ATC	192
56	Glu Met Val Glu Lys Glu Lys Gln His Leu Pro Ser Asp Asp Tyr Ile	
57	50 55 60	
58		
59	AAG AGA CTT AGA AGT GGA GAT TTG GAT TTG AAT GTT GGA AGA AGA GAT	240
60	Lys Arg Leu Arg Ser Gly Asp Leu Asp Leu Asn Val Gly Arg Arg Asp	
61	65 70 75 80	
62		
63	GCC CTC AAT TGG ATT TGG AAG GCT TGT GAA GTA CAC CAG TTT GGA CCA	288
64	Ala Leu Asn Trp Ile Trp Lys Ala Cys Glu Val His Gln Phe Gly Pro	
65	85 90 95	
66		
67	TTG TGT TTT TGC TTA GCA ATG AAC TAC TTG GAT CGA TTC TTA TCG GTT	336
68	Leu Cys Phe Cys Leu Ala Met Asn Tyr Leu Asp Arg Phe Leu Ser Val	
69	100 105 110	
70		
71	CAT GAT TTG CCT AGT GGC AAA GGT TGG ATA TTG CAG TTG TTG GCT GTG	384
72	His Asp Leu Pro Ser Gly Lys Gly Trp Ile Leu Gln Leu Leu Ala Val	
73	115 120 125	
74		
75	GCT TGT TTA TCA TTG GCA GCC AAA ATT GAA GAA ACT GAA GTT CCA ATG	432
76	Ala Cys Leu Ser Leu Ala Ala Lys Ile Glu Glu Thr Glu Val Pro Met	
77	130 135 140	
78		
79	TTG ATA GAT CTT CAG GTT GGA GAT CCT CAG TTT GTG TTT GAG GCT AAA	480
80	Leu Ile Asp Leu Gln Val Gly Asp Pro Gln Phe Val Phe Glu Ala Lys	
81	145 150 155 160	
82		
83	TCA GTC CAA AGA ATG GAG CTT TTG GTG TTG AAC AAA TTG AAA TGG AGA	528
84	Ser Val Gln Arg Met Glu Leu Leu Val Leu Asn Lys Leu Lys Trp Arg	
85	165 170 175	
86		
87	TTG AGA GCA ATA ACT CCA TGC TCA TAC ATA AGA TAT TTC CTG AGA AAG	576
88	Leu Arg Ala Ile Thr Pro Cys Ser Tyr Ile Arg Tyr Phe Leu Arg Lys	
89	180 185 190	
90		
91	ATG AGT AAA TGT GAT CAA GAA CCA TCC AAC ACA TTG ATA TCT AGA TCA	624
92	Met Ser Lys Cys Asp Gln Glu Pro Ser Asn Thr Leu Ile Ser Arg Ser	
93	195 200 205	
94		
95	TTA CAA GTG ATA GCC AGC ACA ACC AAA GGT ATT GAC TTT TTG GAG TTT	672
96	Leu Gln Val Ile Ala Ser Thr Thr Lys Gly Ile Asp Phe Leu Glu Phe	
97	210 215 220	
98		
99	AGA CCT TCT GAA GCT GCT GCT GCT GTG GCA CTT TCT GTT TCT GGA GAA	720

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/530,209

DATE: 02/27/2001  
TIME: 20:20:23

INPUT SET: S36432.raw

```

100 Arg Pro Ser Glu Ala Ala Ala Val Ala Leu Ser Val Ser Gly Glu
101 225                230                235                240
102
103 TTG CAG AGA GTA CAC TTT GAC AAC TCT TCC TTC TCT CCT CTT TTC TCA      768
104 Leu Gln Arg Val His Phe Asp Asn Ser Ser Phe Ser Pro Leu Phe Ser
105                245                250                255
106
107 CTA CTT CAA AAG GAG AGA GTG AAG AAG ATA GGG GAA ATG ATA GAG AGT      816
108 Leu Leu Gln Lys Glu Arg Val Lys Lys Ile Gly Glu Met Ile Glu Ser
109                260                265                270
110
111 GAT GGC TCA GAC TTA TGT TCA CAA ACA CCC AAT GGG GTT TTA GAA GTA      864
112 Asp Gly Ser Asp Leu Cys Ser Gln Thr Pro Asn Gly Val Leu Glu Val
113                275                280                285
114
115 TCG GCT TGT TGT TTC AGC TTT AAG ACC CAT GAT TCT TCT TCT TCT TAT      912
116 Ser Ala Cys Cys Phe Ser Phe Lys Thr His Asp Ser Ser Ser Ser Tyr
117                290                295                300
118
119 ACA CAT CTT TCT TAA      927
120 Thr His Leu Ser *
121 305
122
123
124 (2) INFORMATION FOR SEQ ID NO: 2:
125
126 (i) SEQUENCE CHARACTERISTICS:
127 (A) LENGTH: 308 amino acids
128 (B) TYPE: amino acid
129 (D) TOPOLOGY: linear
130
131 (ii) MOLECULE TYPE: protein
132 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
133
134 Met Ala Glu Glu Asn Leu Glu Leu Ser Leu Leu Cys Thr Glu Ser Asn
135 1                5                10                15
136
137 Val Asp Asp Glu Gly Met Ile Val Asp Glu Thr Pro Ile Glu Ile Ser
138                20                25                30
139
140 Ile Pro Gln Met Gly Phe Ser Gln Ser Glu Ser Glu Glu Ile Ile Met
141                35                40                45
142
143 Glu Met Val Glu Lys Glu Lys Gln His Leu Pro Ser Asp Asp Tyr Ile
144                50                55                60
145
146 Lys Arg Leu Arg Ser Gly Asp Leu Asp Leu Asn Val Gly Arg Arg Asp
147 65                70                75                80
148
149 Ala Leu Asn Trp Ile Trp Lys Ala Cys Glu Val His Gln Phe Gly Pro
150                85                90                95
151
152 Leu Cys Phe Cys Leu Ala Met Asn Tyr Leu Asp Arg Phe Leu Ser Val

```

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/530,209

DATE: 02/27/2001  
TIME: 20:20:23

INPUT SET: S36432.raw

	100	105	110
153			
154			
155	His Asp Leu Pro Ser Gly Lys	Gly Trp Ile Leu Gln	Leu Leu Ala Val
156	115	120	125
157			
158	Ala Cys Leu Ser Leu Ala Ala	Lys Ile Glu Glu Thr	Glu Val Pro Met
159	130	135	140
160			
161	Leu Ile Asp Leu Gln Val Gly Asp	Pro Gln Phe Val Phe	Glu Ala Lys
162	145	150	155
163			
164	Ser Val Gln Arg Met Glu Leu Leu Val	Leu Asn Lys Leu Lys	Trp Arg
165	165	170	175
166			
167	Leu Arg Ala Ile Thr Pro Cys Ser	Tyr Ile Arg Tyr Phe	Leu Arg Lys
168	180	185	190
169			
170	Met Ser Lys Cys Asp Gln Glu Pro	Ser Asn Thr Leu Ile Ser	Arg Ser
171	195	200	205
172			
173	Leu Gln Val Ile Ala Ser Thr Thr	Lys Gly Ile Asp Phe	Leu Glu Phe
174	210	215	220
175			
176	Arg Pro Ser Glu Ala Ala Ala Ala	Val Ala Leu Ser Val Ser	Gly Glu
177	225	230	235
178			
179	Leu Gln Arg Val His Phe Asp Asn	Ser Ser Phe Ser Pro Leu	Phe Ser
180	245	250	255
181			
182	Leu Leu Gln Lys Glu Arg Val Lys	Lys Ile Gly Glu Met Ile	Glu Ser
183	260	265	270
184			
185	Asp Gly Ser Asp Leu Cys Ser Gln	Thr Pro Asn Gly Val Leu	Glu Val
186	275	280	285
187			
188	Ser Ala Cys Cys Phe Ser Phe Lys	Thr His Asp Ser Ser Ser	Ser Tyr
189	290	295	300
190			
191	Thr His Leu Ser		
192	305		
193			
194			

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/530,209DATE: 02/27/2001  
TIME: 20:20:23

INPUT SET: S36432.raw

206 (iii) HYPOTHETICAL: YES  
207  
208 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
209  
210 GAACACTCGA GTGTAATGGC AGAGG 25  
211  
212  
213  
214 (2) INFORMATION FOR SEQ ID NO: 4:  
215  
216 (i) SEQUENCE CHARACTERISTICS:  
217 (A) LENGTH: 25  
218 (B) TYPE: nucleic acid  
219 (C) STRANDEDNESS: single  
220 (D) TOPOLOGY: linear  
221  
222 (ii) MOLECULE TYPE: other nucleic acid  
223 (A) DESCRIPTION: /desc = "oligonucleotide"  
224  
225 (iii) HYPOTHETICAL: YES  
226  
227 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
228  
229 CATCATACTA GTTATAATAA TGTAAG 26  
230

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 309 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

308

(see next page)

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met	Ala	Glu	Glu	Asn	Leu	Glu	Leu	Ser	Leu	Leu	Cys	Thr	Glu	Ser	Asn	
1				5					10					15		
Val	Asp	Asp	Glu	Gly	Met	Ile	Val	Asp	Glu	Thr	Pro	Ile	Glu	Ile	Ser	
			20					25					30			
Ile	Pro	Gln	Met	Gly	Phe	Ser	Gln	Ser	Glu	Ser	Glu	Glu	Ile	Ile	Met	
		35					40					45				
Glu	Met	Val	Glu	Lys	Glu	Lys	Gln	His	Leu	Pro	Ser	Asp	Asp	Tyr	Ile	
	50					55					60					
Lys	Arg	Leu	Arg	Ser	Gly	Asp	Leu	Asp	Leu	Asn	Val	Gly	Arg	Arg	Asp	
	65				70					75					80	
Ala	Leu	Asn	Trp	Ile	Trp	Lys	Ala	Cys	Glu	Val	His	Gln	Phe	Gly	Pro	
				85					90					95		
Leu	Cys	Phe	Cys	Leu	Ala	Met	Asn	Tyr	Leu	Asp	Arg	Phe	Leu	Ser	Val	
			100					105					110			
His	Asp	Leu	Pro	Ser	Gly	Lys	Gly	Trp	Ile	Leu	Gln	Leu	Leu	Ala	Val	
		115					120					125				
Ala	Cys	Leu	Ser	Leu	Ala	Ala	Lys	Ile	Glu	Glu	Thr	Glu	Val	Pro	Met	
	130					135					140					
Leu	Ile	Asp	Leu	Gln	Val	Gly	Asp	Pro	Gln	Phe	Val	Phe	Glu	Ala	Lys	
	145				150					155					160	
Ser	Val	Gln	Arg	Met	Glu	Leu	Leu	Val	Leu	Asn	Lys	Leu	Lys	Trp	Arg	
				165					170					175		
Leu	Arg	Ala	Ile	Thr	Pro	Cys	Ser	Tyr	Ile	Arg	Tyr	Phe	Leu	Arg	Lys	
			180					185					190			
Met	Ser	Lys	Cys	Asp	Gln	Glu	Pro	Ser	Asn	Thr	Leu	Ile	Ser	Arg	Ser	
		195					200					205				
Leu	Gln	Val	Ile	Ala	Ser	Thr	Thr	Lys	Gly	Ile	Asp	Phe	Leu	Glu	Phe	
	210					215					220					
Arg	Pro	Ser	Glu	Ala	Ala	Ala	Ala	Val	Ala	Leu	Ser	Val	Ser	Gly	Glu	
	225				230					235					240	
Leu	Gln	Arg	Val	His	Phe	Asp	Asn	Ser	Ser	Phe	Ser	Pro	Leu	Phe	Ser	
				245					250					255		
Leu	Leu	Gln	Lys	Glu	Arg	Val	Lys	Lys	Ile	Gly	Glu	Met	Ile	Glu	Ser	
			260					265						270		

08/530,209

7

Asp Gly Ser Asp Leu Cys Ser Gln Thr Pro Asn Gly Val Leu Glu Val  
275 280 285

Ser Ala Cys Cys Phe Ser Phe Lys Thr His Asp Ser Ser Ser Ser Tyr  
290 295 300

Thr His Leu Ser  
305

(\*) delete ending stop codon



**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/09/530,209**DATE: 02/27/2001  
TIME: 20:20:24**INPUT SET: S36432.raw**

Line	Error	Original Text
5	Mandatory Value Not Present	(i) APPLICANT:
6	Unknown or Misplaced Identifier	(A) NAME: CropDesign NV
7	Unknown or Misplaced Identifier	(B) STREET: TechnologiePark Zwijnaarde 3
8	Unknown or Misplaced Identifier	(C) CITY: Gent
9	Unknown or Misplaced Identifier	(D) STATE: none
10	Unknown or Misplaced Identifier	(E) COUNTRY: Belgium
11	Unknown or Misplaced Identifier	(F) POSTAL CODE (ZIP): 9052
195	Stop Codon at end of sequence removed - no error	(2) INFORMATION FOR SEQ ID NO: 3:

PAGE: 1

**SEQUENCE MISSING ITEM REPORT**  
**PATENT APPLICATION US/09/530,209**

DATE: 02/27/2001  
TIME: 20:20:24

***INPUT SET: S36432.raw***

ADDRESSEE  
STREET  
CITY  
STATE  
COUNTRY  
ZIP  
CORRESPONDENCE ADDRESS  
APPLICATION NUMBER  
FILING DATE  
CLASSIFICATION  
CURRENT APPLICATION DATA  
APPLICATION NUMBER  
FILING DATE  
PRIOR APPLICATION DATA